

carbohydrates or enzymes.

Claim 20; Page 244-245; 1246pp; English.

AA71360 to AA71750 encode the Corynebacterium glutamicum sugar metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteoglycan or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polypeptide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diptheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to C. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).

Sequence 425 AA:

Query Match 99.5%; Score 2145; DB 4; Length 425;
Best Local Similarity 99.5%; Pred. No. 8.1e-169;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEAHELRDGGDRYL	60
DB	1	VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEAHELRDGGDRYL	60
QY	61	KGVLKAVENNEEIGDELAGEADDRILDEAMIKLDTANKSRILGANILGSMVAVAKA	120
DB	61	KGVLKAVENNEEIGDELAGEADDRILDEAMIKLDTANKSRILGANILGSMVAVAKA	120
QY	121	AADSAGLPLFRYIGGPNNAVLVPMNMIIINGGAHDSGVDOEFMIAPIGAEFTSEALRN	180
DB	121	AADSAGLPLFRYIGGPNNAVLVPMNMIIINGGAHDSGVDOEFMIAPIGAEFTSEALRN	180
QY	181	GAEVTHALKSVYKEKGLSTGIDGEGFAPSVGSTREALDLIVAKIEXAGTTPGKIDIAL	240
DB	181	GAEVTHALKSVYKEKGLSTGIDGEGFAPSVGSTREALDLIVAKIEXAGTTPGKIDIAL	240
QY	241	DVASSEFKDGTTHFEGGSHSAEMANVYAEVLDAYIVSIEDPLDEDDWEGYTNLTAT	300
DB	241	DVASSEFKDGTTHFEGGSHSAEMANVYAEVLDAYIVSIEDPLDEDDWEGYTNLTAT	300
QY	301	GDKVOIVGDDPFVYTNPERLKEGIAKKAANSILVKNQIGLTETPDADVMAHAGTTSNM	360
DB	301	GDKVOIVGDDPFVYTNPERLKEGIAKKAANSILVKNQIGLTETPDADVMAHAGTTSNM	360
QY	361	SHRSGETEDTTIADLAVANCGOIKTGAPASDRVAKYNQLEQLLGGAGVYAGRSAP	420
DB	361	SHRSGETEDTTIADLAVANCGOIKTGAPASDRVAKYNQLEQLLGGAGVYAGRSAP	420
QY	421	PRFQG 425	
DB	421	PRFQG 425	

RESULT 5

ADD13323 ID ADD13323 standard; protein: 425 AA.

ADD13323;

01-JAN-2004 (first entry)

C. glutamicum carbon metabolism associated protein RKA00235.

carbon metabolism; energy-rich molecule; oxidative phosphorylation;

fine chemical; amino acid production; lysine production; nucleotide production; nucleoside production; lipid production; fatty acid production; diol production; carbohydrate production; aromatic compound production; vitamin production; co-factor production; enzyme production; food; animal feed; cosmetic; pharmaceutical.

Corynebacterium glutamicum.

Key Location/Qualifiers

FT M8c difference 223 /note="Optionally substituted with Lys"

PN WO2003040291-A2.

PD 15-MAY-2003.

PF 31-OCT-2002, 2002MO-EP012135.

PR 05-NOV-2001, 2001DE-01054270.

PA (BADI) BASF AG.

PI Zelder O, Pompejus M, Schroeder H, Kroeger B, Kloppege C;

PI Haberman G;

DR WPI: 2003-505068/47.

DR N-PSDB; ADD13322.

FT New nucleic acid encoding variant forms of proteins involved in carbon

FT compound metabolism, useful for production of fine chemicals,

FT specifically lysine, in microorganisms.

PS Claim 1; SEQ ID NO 8; 259pp; German.

This invention describes novel polynucleotides and polypeptides associated with the metabolism of carbon compounds and generation of energy-rich molecules by oxidative phosphorylation in Corynebacterium glutamicum. The polynucleotides of the invention are isolated from a nucleic acid library of C. glutamicum then mutated at the specified positions, cloned and expressed by standard methods. Cells, especially Corynebacterium glutamicum, containing vectors that express the polynucleotides are used for production of fine chemicals, preferably amino acids and specifically lysine, but more generally nucleotides, nucleosides, lipids, fatty acids, diols, carbohydrates, aromatic compounds, vitamins, co-factors and enzymes. These are useful in the food, animal feed, cosmetics and pharmaceutical industries. CC Polynucleotides, optionally as primers and probes, can also be used for identification and classification of C. glutamicum and related species, CC e.g. for diagnosis; for genomic mapping; functional or evolutionary CC studies gene manipulation, and modulation of metabolic activity. Cells CC that contain the products of the invention may produce fine chemicals in CC better yields, with higher productivity and/or more efficiently.

Sequence 425 AA:

Query Match 99.5%; Score 2145; DB 7; Length 425;
Best Local Similarity 99.5%; Pred. No. 8.1e-169;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEAHELRDGGDRYL	60
DB	1	VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEAHELRDGGDRYL	60
QY	61	KGVLKAVENNEEIGDELAGEADDRILDEAMIKLDTANKSRILGANILGSMVAVAKA	120
DB	61	KGVLKAVENNEEIGDELAGEADDRILDEAMIKLDTANKSRILGANILGSMVAVAKA	120
QY	121	AADSAGLPLFRYIGGPNNAVLVPMNMIIINGGAHDSGVDOEFMIAPIGAEFTSEALRN	180
DB	121	AADSAGLPLFRYIGGPNNAVLVPMNMIIINGGAHDSGVDOEFMIAPIGAEFTSEALRN	180
QY	181	GAEVTHALKSVYKEKGLSTGIDGEGFAPSVGSTREALDLIVAKIEXAGTTPGKIDIAL	240
DB	181	GAEVTHALKSVYKEKGLSTGIDGEGFAPSVGSTREALDLIVAKIEXAGTTPGKIDIAL	240

XX WO2003023016-A2.
 XX 20-MAR-2003.
 PD 11-SEP-2002; 2002WO-EP010174.
 XX 13-SEP-2001; 2001DE-01045043.
 XX (DEGS) DEGUSA AG.
 PA Farwick M, Hermann T;
 PI WPI; 2003-354534/33.
 DR N-PSDB; ACC45311.
 XX Microorganism useful for producing e.g. fine chemicals, has permanently
 PT altered phosphorylatability protein, such that biosynthesis of fine
 PT chemical synthesized by microorganism is increased compared to wild-type.
 XX
 PS Example 3; Page 80-81; 120pp; English.
 XX
 CC The present invention describes a microorganism (I), in which the
 CC phosphorylatability of at least one protein has been permanently altered
 CC such that the biosynthesis of at least one fine chemical synthesized by
 CC the microorganism is increased compared to the wild type. Also described:
 CC (1) use of a DNA (II) sequence coding for a protein which contains a
 CC phosphorylation site, where the sequence contains such a mutation that
 CC the protein is changed in its phosphorylatability for the production of
 CC (1), or for the production of fine chemicals; and (2) a method for
 CC producing fine chemicals or metabolites comprising using (I). (I) is
 CC useful for producing fine chemicals or metabolites, such as amino acids,
 CC vitamins, nucleosides, nucleotides, pigments or proteins. The amino acids
 CC and vitamins produced using (I) can be used in human medicine, in the
 CC pharmaceutical industry, food industry and in animal feeding. (I)
 CC produces larger amount of desired fine chemical or a metabolite than the
 CC wild type. The present sequence represents wild type and from
 CC Corynebacterium glutamicum, which is used in an example from the present
 CC invention
 CC
 XX Sequence 425 AA;
 SQ
 Query March 99.7%; Score 2148; DB 6; Length 425;
 Best Local Similarity 99.5%; Pred. No. 1,5e-169;
 Matches 423; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VAEIMHFAEILDSRGNPTVEAEVFLDDSGHGVGVSQSTGVHEAHELRDGGRRYIG 60
 DB 1 MAEIMHFAEILDSRGNPTVEAEVFLDDSGHGVGVSQSTGVHEAHELRDGGRRYIG 60
 QY 61 KGVIAKAVENVEETIGDELAGEADDOQLIDEAMIKLGNKRLGNALIGVSMVAQA 120
 DB 61 KGVIAKAVENVEETIGDELAGEADDOQLIDEAMIKLGNKRLGNALIGVSMVAQA 120
 QY 121 AADAGCPLPRYIGGPNANHVPVPMNNIINGGAADSGVVOEMTAPCAETFESEALRN 180
 DB 121 AADAGCPLPRYIGGPNANHVPVPMNNIINGGAADSGVVOEMTAPCAETFESEALRN 180
 QY 181 GAEVYHLLKSVIKKKGSTGIDEGGFAPSVGSRTREALDIIYVAIEKAGTTPGKDIALAL 240
 DB 181 GAEVYHLLKSVIKKKGSTGIDEGGFAPSVGSRTREALDIIYVAIEKAGTTPGKDIALAL 240
 QY 241 DVASSEFFKDTYHFEFGQSHSAEMANYAELVDAYIVISIEDPLQEDDMEGTNTNATI 300
 DB 241 DVASSEFFKDTYHFEFGQSHSAEMANYAELVDAYIVISIEDPLQEDDMEGTNTNATI 300
 QY 301 GDKVOIVDDDFVNNPEIKKGIKKAANSTLVVNOIGTLTFEFDVDMAHKAGTSMK 360
 DB 301 GDKVOIVDDDFVNNPEIKKGIKKAANSTLVVNOIGTLTFEFDVDMAHKAGTSMK 360
 QY 361 SHRSGETEDTTIADLAVANLNGQIKTGAPARSDVAVAKYNOLLRIEQLLDGAGVYAGRSAP 420
 DB 361 SHRSGETEDTTIADLAVANLNGQIKTGAPARSDVAVAKYNOLLRIEQLLDGAGVYAGRSAP 420

QY 421 PRFOG 425
 DB 421 PRFOG 425
 RESULT 4
 AAB79278
 ID AAB79278 standard; protein; 425 AA.
 XX
 AC AAB79278;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Corynebacterium glutamicum SMP protein sequence SEQ ID NO:72.
 XX
 KW Corynebacterium glutamicum; carbon metabolism and energy production;
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
 KW fine chemical production; organic acid; proteinogenic amino acid;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polypeptide; enzyme;
 KW diagnosis; Corynebacterium diptheriae; evolutionary study.
 KW
 OS Corynebacterium glutamicum.
 XX
 PN WO200100844-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 23-JUN-2000; 2000WO-IB000943.
 XX
 PR 25-JUN-1999; 99US-0141031P.
 PR 08-JUL-1999; 99DE-01031412.
 PR 08-JUL-1999; 99DE-01031413.
 PR 08-JUL-1999; 99DE-01031419.
 PR 08-JUL-1999; 99DE-01031420.
 PR 08-JUL-1999; 99DE-01031424.
 PR 08-JUL-1999; 99DE-01031428.
 PR 08-JUL-1999; 99DE-01031431.
 PR 08-JUL-1999; 99DE-01031433.
 PR 08-JUL-1999; 99DE-01031434.
 PR 08-JUL-1999; 99DE-01031510.
 PR 08-JUL-1999; 99DE-01031562.
 PR 08-JUL-1999; 99DE-01031634.
 PR 09-JUL-1999; 99DE-01032180.
 PR 09-JUL-1999; 99DE-01032227.
 PR 09-JUL-1999; 99DE-01032230.
 PR 09-JUL-1999; 99US-0143208P.
 PR 14-JUL-1999; 99DE-01032924.
 PR 14-JUL-1999; 99DE-01032973.
 PR 14-JUL-1999; 99DE-01033005.
 PR 14-JUL-1999; 99DE-01040765.
 PR 27-AUG-1999; 99US-0151572P.
 PR 31-AUG-1999; 99DE-01042076.
 PR 03-SEP-1999; 99DE-01042079.
 PR 03-SEP-1999; 99DE-01042086.
 PR 03-SEP-1999; 99DE-01042087.
 PR 03-SEP-1999; 99DE-01042088.
 PR 03-SEP-1999; 99DE-01042095.
 PR 03-SEP-1999; 99DE-01042123.
 PR 03-SEP-1999; 99DE-01042125.
 XX
 PA (BADI) BASF AG.
 XX
 PI Pompejus M, Kroeger B, Schroeder H, Zeidler O, Haberhauer G;
 XX WPI; 2001-061975/07.
 DR N-PSDB; AAF71395.
 XX
 PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 PT metabolism and oxidative phosphorylation protein for production or
 PT modulation of production of fine chemicals e.g. amino acids,

FEATURES BASF AKTIENSELLSCHAF (DE)
Location/Qualifiers
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/db_xref="taxon:1718"
101..1378
/note="unnamed protein product; RXA00235"

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VQFMPIPIGAETSEBALRNGAEVHALKSVIKEGLSTGLDEGGFAVSSTREAL
DIVEIAIEKAFPGKDIALDVAASSEFKDGYHFEQSGHSAEMNAVVELDAY
PIVISEDPLQEDMDGVTNLTATIGDKVOIGDDFVTPERLKEGIAKKAANSLIVK
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ORIGIN

Query Match 88.4%; Score 1394.8; DB 6; Length 1398;
Best Local Similarity 99.9%; Pred. No. 1.9e-254;
Matches 1396; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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1 CGAACAAGATTCGTGCACATTTGGGTGATGAGATTTGAAGACATTTGATCAGTGA 60
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121 ATTGCTCGGGAATTCGACATCCCGCGGTAAACCAACCGTGGAGGACAGATTTCTT 180
231 GGATGACGATTCACGAGGTGCGCAGGTGTTTCATCCGCGCATCCACGCGGTCCACGA 290
181 GGATGACGATTCACGAGGTGCGCAGGTGTTTCATCCGCGCATCCACGCGGTCCACGA 240
291 GGCTCATGAGCTGCGTGAACGCTGCGATCGTACCTGCGCAAGGCGCTTTGAAGGACGT 350
241 GGCTCATGAGCTGCGTGAACGCTGCGATCGTACCTGCGCAAGGCGCTTTGAAGGACGT 300
351 TGAAGAAGTCAACGAAGAAATCGGCGAAGAGCTGCGCTAGAGGCTGACATCAGCG 410
301 TGAAGAAGTCAACGAAGAAATCGGCGAAGAGCTGCGCTAGAGGCTGACATCAGCG 360
411 CCTGATGAGAGCAATGATCAAGCTTGATGAGCACCAGCAAGTCCCGCTGGGTGC 470
361 CCTGATGAGAGCAATGATCAAGCTTGATGAGCACCAGCAAGTCCCGCTGGGTGC 420
471 AAAGCAATCCTTGGTGTTCATGAGCTGTTGCAAAAGGCTGCTGCTGATTCGCAAGGCT 530
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891 CTTCAAGAGCGGACCTACCACTTCGAAGGTGGCAGACACTCGGACCTGAGATGCGAAA 950
841 CTTCAAGAGCGGACCTACCACTTCGAAGGTGGCAGACACTCGGACCTGAGATGCGAAA 900
951 CGTTACGCTGAGTCTGTTGACGGCTAACCCATGCTCTCATTCGAGAACCCACTGCGAGA 1010
901 CGTTACGCTGAGTCTGTTGACGGCTAACCCATGCTCTCATTCGAGAACCCACTGCGAGA 960
1011 AGATGACTGGAGGCTTACACCAACCTTCACCGGCAACCACTCGGCGAAGGTTGAGATGCT 1070
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1431 AAAAGCGCTTTCGACGC 1448
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RESULT 10
BD163286 1275 bp DNA linear PAT 17-JAN-2003
IDCS BD163286
DEFINITION Novel polynucleotide.
ACCESSION BD163286
VERSION BD163286.1 GI:27869050
KEYWORDS JP 2002191370-A/1085.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 1275)
AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,A.
TITLE Novel polynucleotide
JOURNAL Patent: JP 2002191370-A 1085 09-JUL-2002;
KYOMA HAKKO KOGYO CO LTD
OS Corynebacterium glutamicum
PN JP 2002191370-A/1085
PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
KEIKO OCHIAI,
PI HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO

REFERENCE

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Zelder, O., Pompejus, M., Schroeder, H., Kroege, B., Kloppe, C. and
Haberhauser, G.
Genes encoding for carbon metabolism and energy-producing proteins
Patent: WO 03040291-A 7 15-MAY-2003;
JOURNAL BASF AKTIENGESellschaft (DE)

FEATURES

SOURCE

CDS

1. 1405
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ORIGIN

Query Match 88.8%; Score 1401.8; DB 6; Length 1405;
Best Local Similarity 99.9%; Pred. No. 9.1e-256;
Matches 1403; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 9
AX064945
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Pompejus, M., Kroege, B., Schroeder, H., Zelder, O. and Haberhauser, G.
Corynebacterium glutamicum genes encoding proteins involved in
carbon metabolism and energy production
Patent: WO 0100844-A 71 04-JAN-2001;
JOURNAL

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; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: BGI-126CPN
; CURRENT APPLICATION NUMBER: US/10/781.014
; PRIOR FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 09/602,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/143,208
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/151,572
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19931412.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931424.1
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931426.4
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 784
; SEQ ID NO 72
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-10-781-014-72

Query Match          99.7%; Score 2149; DB 16; Length 425;
Best Local Similarity 99.8%; Pred. No. 8.3e-171;
Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEAHELDDGGDRYL 60
DB 1 VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEAHELDDGGDRYL 60
QY 61 KGVKAVENNEEIGDELGLAADDORLIDEAMIKLDGTANKSRIGANAILGVSAVAKA 120
DB 61 KGVKAVENNEEIGDELGLAADDORLIDEAMIKLDGTANKSRIGANAILGVSAVAKA 120
QY 61 KGVKAVENNEEIGDELGLAADDORLIDEAMIKLDGTANKSRIGANAILGVSAVAKA 120
DB 61 KGVKAVENNEEIGDELGLAADDORLIDEAMIKLDGTANKSRIGANAILGVSAVAKA 120
QY 121 AADSGAPLPRFYIGGNPAHVLPVPMNITINGGAHDSGVDOEPMIAPIGATFSSALRN 180
DB 121 AADSGAPLPRFYIGGNPAHVLPVPMNITINGGAHDSGVDOEPMIAPIGATFSSALRN 180
QY 121 AADSGAPLPRFYIGGNPAHVLPVPMNITINGGAHDSGVDOEPMIAPIGATFSSALRN 180
DB 121 AADSGAPLPRFYIGGNPAHVLPVPMNITINGGAHDSGVDOEPMIAPIGATFSSALRN 180
QY 181 GAEVYHALKSVYKKEKGLSTGLDEGGFAPS VGSTREALDLIVEAIEKAGFTFGKDIALL 240
DB 181 GAEVYHALKSVYKKEKGLSTGLDEGGFAPS VGSTREALDLIVEAIEKAGFTFGKDIALL 240
QY 181 GAEVYHALKSVYKKEKGLSTGLDEGGFAPS VGSTREALDLIVEAIEKAGFTFGKDIALL 240
DB 181 GAEVYHALKSVYKKEKGLSTGLDEGGFAPS VGSTREALDLIVEAIEKAGFTFGKDIALL 240
QY 241 DVASSEFFKDTYFEGGQSHAAEMANVVAELVDAYIVISIEDPLQEDDMEGYTNLTATI 300
DB 241 DVASSEFFKDTYFEGGQSHAAEMANVVAELVDAYIVISIEDPLQEDDMEGYTNLTATI 300
QY 241 DVASSEFFKDTYFEGGQSHAAEMANVVAELVDAYIVISIEDPLQEDDMEGYTNLTATI 300
DB 241 DVASSEFFKDTYFEGGQSHAAEMANVVAELVDAYIVISIEDPLQEDDMEGYTNLTATI 300
QY 301 GDKVQIVGDDEFVTNPERLKEGIAKKAANSILVKNQOIGLTETFPDAVMAHRAGYTSM 360
DB 301 GDKVQIVGDDEFVTNPERLKEGIAKKAANSILVKNQOIGLTETFPDAVMAHRAGYTSM 360
QY 301 GDKVQIVGDDEFVTNPERLKEGIAKKAANSILVKNQOIGLTETFPDAVMAHRAGYTSM 360
DB 301 GDKVQIVGDDEFVTNPERLKEGIAKKAANSILVKNQOIGLTETFPDAVMAHRAGYTSM 360
QY 361 SHRSGETEDTTIADLAVALNCGOIKTGAPARSDRVAKYNQDLRIEQLLDGAGVYAGRS 420
DB 361 SHRSGETEDTTIADLAVALNCGOIKTGAPARSDRVAKYNQDLRIEQLLDGAGVYAGRS 420
QY 361 SHRSGETEDTTIADLAVALNCGOIKTGAPARSDRVAKYNQDLRIEQLLDGAGVYAGRS 420
DB 361 SHRSGETEDTTIADLAVALNCGOIKTGAPARSDRVAKYNQDLRIEQLLDGAGVYAGRS 420
QY 421 PRFQG 425
DB 421 PRFQG 425

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; GENERAL INFORMATION:
; APPLICANT: Zeider, Oskar
; APPLICANT: Pompejus, Markus
; APPLICANT: Schroder, Hartwig
; APPLICANT: Krieger, Burkhard
; APPLICANT: Klopptogge, Corinna
; APPLICANT: Habernauer, Gregor
; TITLE OF INVENTION: Genes coding for proteins of carbon metabolism and energy produc
; FILE REFERENCE: BGI-167US
; CURRENT APPLICATION NUMBER: US/10/494,836
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: PCT/EP02/12135
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: DE 101 54 270.4
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-10-494-836-8

Query Match          99.7%; Score 2149; DB 17; Length 425;
Best Local Similarity 99.8%; Pred. No. 8.3e-171;
Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEAHELDDGGDRYL 60
DB 1 VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEAHELDDGGDRYL 60
QY 61 KGVKAVENNEEIGDELGLAADDORLIDEAMIKLDGTANKSRIGANAILGVSAVAKA 120
DB 61 KGVKAVENNEEIGDELGLAADDORLIDEAMIKLDGTANKSRIGANAILGVSAVAKA 120
QY 61 KGVKAVENNEEIGDELGLAADDORLIDEAMIKLDGTANKSRIGANAILGVSAVAKA 120
DB 61 KGVKAVENNEEIGDELGLAADDORLIDEAMIKLDGTANKSRIGANAILGVSAVAKA 120
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DB 121 AADSGAPLPRFYIGGNPAHVLPVPMNITINGGAHDSGVDOEPMIAPIGATFSSALRN 180
QY 121 AADSGAPLPRFYIGGNPAHVLPVPMNITINGGAHDSGVDOEPMIAPIGATFSSALRN 180
DB 121 AADSGAPLPRFYIGGNPAHVLPVPMNITINGGAHDSGVDOEPMIAPIGATFSSALRN 180
QY 181 GAEVYHALKSVYKKEKGLSTGLDEGGFAPS VGSTREALDLIVEAIEKAGFTFGKDIALL 240
DB 181 GAEVYHALKSVYKKEKGLSTGLDEGGFAPS VGSTREALDLIVEAIEKAGFTFGKDIALL 240
QY 181 GAEVYHALKSVYKKEKGLSTGLDEGGFAPS VGSTREALDLIVEAIEKAGFTFGKDIALL 240
DB 181 GAEVYHALKSVYKKEKGLSTGLDEGGFAPS VGSTREALDLIVEAIEKAGFTFGKDIALL 240
QY 241 DVASSEFFKDTYFEGGQSHAAEMANVVAELVDAYIVISIEDPLQEDDMEGYTNLTATI 300
DB 241 DVASSEFFKDTYFEGGQSHAAEMANVVAELVDAYIVISIEDPLQEDDMEGYTNLTATI 300
QY 241 DVASSEFFKDTYFEGGQSHAAEMANVVAELVDAYIVISIEDPLQEDDMEGYTNLTATI 300
DB 241 DVASSEFFKDTYFEGGQSHAAEMANVVAELVDAYIVISIEDPLQEDDMEGYTNLTATI 300
QY 301 GDKVQIVGDDEFVTNPERLKEGIAKKAANSILVKNQOIGLTETFPDAVMAHRAGYTSM 360
DB 301 GDKVQIVGDDEFVTNPERLKEGIAKKAANSILVKNQOIGLTETFPDAVMAHRAGYTSM 360
QY 301 GDKVQIVGDDEFVTNPERLKEGIAKKAANSILVKNQOIGLTETFPDAVMAHRAGYTSM 360
DB 301 GDKVQIVGDDEFVTNPERLKEGIAKKAANSILVKNQOIGLTETFPDAVMAHRAGYTSM 360
QY 361 SHRSGETEDTTIADLAVALNCGOIKTGAPARSDRVAKYNQDLRIEQLLDGAGVYAGRS 420
DB 361 SHRSGETEDTTIADLAVALNCGOIKTGAPARSDRVAKYNQDLRIEQLLDGAGVYAGRS 420
QY 361 SHRSGETEDTTIADLAVALNCGOIKTGAPARSDRVAKYNQDLRIEQLLDGAGVYAGRS 420
DB 361 SHRSGETEDTTIADLAVALNCGOIKTGAPARSDRVAKYNQDLRIEQLLDGAGVYAGRS 420
QY 421 PRFQG 425
DB 421 PRFQG 425

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RESULT 7
 US-10-494-836-8
 ; Sequence 8, Application: US/10494836
 ; Publication No. US2005001423A1

RESULT 8
 US-10-282-1226-53908
 ; Sequence 53908, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant

Db 301 GDKVQIVGDDFFVTNPRLEKEGIKKAANSILVKNQIGLTFEPDAVMAHRAGYTSM 360
Qy 361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRAVAKYNOLLRIEQLLGAGVYAGRSAR 420
Db 361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRAVAKYNOLLRIEQLLGAGVYAGRSAR 420
Qy 421 PRFOG 425
Db 421 PRFOG 425
RESULT 4
US-09-860-768-4
Sequence 4, Application US/09860768
Patent No. US20020082403A1
GENERAL INFORMATION:
APPLICANT: Mockel, Bettina
APPLICANT: Pfeifferle, Walter
APPLICANT: Hermann, Thomas
APPLICANT: Pohler, Alfred
APPLICANT: Kalinowski, Jörn
APPLICANT: Bathe, Brigitte
TITLE OF INVENTION: New Nucleotide Sequences that Code for the Eno Gene
FILE REFERENCE: 21123/278404
CURRENT APPLICATION NUMBER: US/09/860,768
PRIORITY FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 425
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-860-768-4
Query Match 99.8%; Score 2151; DB 9; Length 425;
Best Local Similarity 99.8%; Pred. No. 5,6e-171;
Matches 424; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEHRLDGGDRYL 60
Db 1 VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEHRLDGGDRYL 60
Qy 61 KGVKAVENNEBEIGDELGLADDDORLIDEAMIKLDTANKSRIGANAILGVSMVAKA 120
Db 61 KGVKAVENNEBEIGDELGLADDDORLIDEAMIKLDTANKSRIGANAILGVSMVAKA 120
Qy 121 AADSAGLPLFRYIGGPNNAHLVPWMNIINGGAHDSGVDOEFMIAPIGAETFESEALRN 180
Db 121 AADSAGLPLFRYIGGPNNAHLVPWMNIINGGAHDSGVDOEFMIAPIGAETFESEALRN 180
Qy 181 GAEVYHALKSVIKEKGLSTGLDEGEGFAPSVGSTREALDLVKAIEKGFPGKDIATL 240
Db 181 GAEVYHALKSVIKEKGLSTGLDEGEGFAPSVGSTREALDLVKAIEKGFPGKDIATL 240
Qy 241 DVASSEFFKDGTYHFEQGHSAEEMANYVAELVDAYPIVISIEDPLQEDDMEGYTNLTATI 300
Db 241 DVASSEFFKDGTYHFEQGHSAEEMANYVAELVDAYPIVISIEDPLQEDDMEGYTNLTATI 300
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Db 301 GDKVQIVGDDFFVTNPRLEKEGIKKAANSILVKNQIGLTFEPDAVMAHRAGYTSM 360
Qy 361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRAVAKYNOLLRIEQLLGAGVYAGRSAR 420
Db 361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRAVAKYNOLLRIEQLLGAGVYAGRSAR 420
Qy 421 PRFOG 425
Db 421 PRFOG 425
RESULT 5

US-10-728-947-4
Sequence 4, Application US/10728947
Publication No. US20040220394A1
GENERAL INFORMATION:
APPLICANT: Mockel, Bettina
APPLICANT: Pfeifferle, Walter
APPLICANT: Hermann, Thomas
APPLICANT: Pohler, Alfred
APPLICANT: Kalinowski, Jörn
APPLICANT: Bathe, Brigitte
TITLE OF INVENTION: New Nucleotide Sequences that Code for the Eno Gene
FILE REFERENCE: 21123/278404
CURRENT APPLICATION NUMBER: US/10/728,947
PRIORITY FILING DATE: 2003-12-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 425
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-10-728-947-4
Query Match 99.8%; Score 2151; DB 16; Length 425;
Best Local Similarity 99.8%; Pred. No. 5,6e-171;
Matches 424; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEHRLDGGDRYL 60
Db 1 VAEIMHVFAREILDSRGNPTVEAEVFLDDSGHGVAGVPSGASTGVHEHRLDGGDRYL 60
Qy 61 KGVKAVENNEBEIGDELGLADDDORLIDEAMIKLDTANKSRIGANAILGVSMVAKA 120
Db 61 KGVKAVENNEBEIGDELGLADDDORLIDEAMIKLDTANKSRIGANAILGVSMVAKA 120
Qy 121 AADSAGLPLFRYIGGPNNAHLVPWMNIINGGAHDSGVDOEFMIAPIGAETFESEALRN 180
Db 121 AADSAGLPLFRYIGGPNNAHLVPWMNIINGGAHDSGVDOEFMIAPIGAETFESEALRN 180
Qy 181 GAEVYHALKSVIKEKGLSTGLDEGEGFAPSVGSTREALDLVKAIEKGFPGKDIATL 240
Db 181 GAEVYHALKSVIKEKGLSTGLDEGEGFAPSVGSTREALDLVKAIEKGFPGKDIATL 240
Qy 241 DVASSEFFKDGTYHFEQGHSAEEMANYVAELVDAYPIVISIEDPLQEDDMEGYTNLTATI 300
Db 241 DVASSEFFKDGTYHFEQGHSAEEMANYVAELVDAYPIVISIEDPLQEDDMEGYTNLTATI 300
Qy 301 GDKVQIVGDDFFVTNPRLEKEGIKKAANSILVKNQIGLTFEPDAVMAHRAGYTSM 360
Db 301 GDKVQIVGDDFFVTNPRLEKEGIKKAANSILVKNQIGLTFEPDAVMAHRAGYTSM 360
Qy 361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRAVAKYNOLLRIEQLLGAGVYAGRSAR 420
Db 361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRAVAKYNOLLRIEQLLGAGVYAGRSAR 420
Qy 421 PRFOG 425
Db 421 PRFOG 425
RESULT 6
US-10-781-014-72
Sequence 72, Application US/10781014
Publication No. US20040180408A1
GENERAL INFORMATION:
APPLICANT: Pompeius, Markus
APPLICANT: Krieger, Burkhard
APPLICANT: Schröder, Hartwig
APPLICANT: Zeider, Oskar
APPLICANT: Habernauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENDOGENY

421 AAGCCATCTGTTGTTTCCATGCTGTTGCAAGAGCTGCTGATTCGAGAGCCT 480
 531 CCCACTGTTCCGCTACATCGGTGACCAAGCAGACGCTTCTCCAGTTCCATGATGAA 590
 481 CCCACTGTTCCGCTACATCGGTGACCAAGCAGACGCTTCTCCAGTTCCATGATGAA 540
 501 CATCATCAACGCTGCGCTCAGCGCTGATCCGGGTGTTACGTTCAAGAAATTCATGATGC 650
 541 CATCATCAACGCTGCGCTCAGCGCTGATCCGGGTGTTACGTTCAAGAAATTCATGATGC 600
 651 TCCATTCGCTGAGAGACCTTCTGAGGCTTCCGCAAGCGCGAGGCTCTACACGC 710
 601 TCCATTCGCTGAGAGACCTTCTGAGGCTTCCGCAAGCGCGAGGCTCTACACGC 660
 711 ACTGAAGTCCGCTCATCAAGAAAGAGCTGTCCACCGAGCTTGCGATGAGGCGGCTT 770
 661 ACTGAAGTCCGCTCATCAAGAAAGAGCTGTCCACCGAGCTTGCGATGAGGCGGCTT 720
 771 CGCTCCTTCCGCTGAGCTCCACCGGTGAGGCTTTCACCTTATCGTTGAGGCAATCGAGA 830
 721 CGCTCCTTCCGCTGAGCTCCACCGGTGAGGCTTTCACCTTATCGTTGAGGCAATCGAGA 780
 831 CGCTGCTTCAACCCAGCAGCAAGAGATCGCTTCTGCTGAGAGCTTCTCTGAGTT 890
 781 GCGTGGCTTCAACCCAGCAGCAAGAGATCGCTTCTGCTGAGAGCTTCTCTGAGTT 840
 891 CTTCAAGAGCGGACCTTCACTTTCGAAAGGTGGAGCAGCACTCCGAGCTGAGATGACAA 950
 841 CTTCAAGAGCGGACCTTCACTTTCGAAAGGTGGAGCAGCACTCCGAGCTGAGATGACAA 900
 951 CGTTTACGCTGAGCTGTTGAGCGGCTGACCAATCGTCTTCATGAGAGACCACTGACAGA 1010
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 1011 AGATGATGAGGAGGTTTACCAACCTTCAACCGCAACATCGGCGCAAGGTTCCATGATGT 1070
 961 AGATGATGAGGAGGTTTACCAACCTTCAACCGCAACATCGGCGCAAGGTTCCATGATGT 1020
 1071 TGGCGAGCCTTCTTCGTCACCAACCTTCAACCGCAACATCGGCGCAAGGTTCCATGATGT 1130
 1021 TGGCGAGCCTTCTTCGTCACCAACCTTCAACCGCAACATCGGCGCAAGGTTCCATGATGT 1080
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 1081 TGGCAATCCTCATCTGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 1140
 1191 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1250
 1141 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 1251 CGAGGACACCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1310
 1201 CGAGGACACCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 1311 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1370
 1261 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 1371 GCTTGGAGAGCGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1430
 1321 GCTTGGAGAGCGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 1431 AAAAGCGCTTTTTCGAGCG 1448
 1381 AAAAGCGCTTTTTCGAGCG 1398

RESULT 8
 US-09-738-626-1085
 ; Sequence 1085, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI
 APPLICANT: MIZOGUCHI, HIROSHI
 APPLICANT: ANDO, SEIKO
 APPLICANT: HAYASHI, MIKIRO
 APPLICANT: OCHIAI, KEIKO
 APPLICANT: YOKOI, HARUHIKO
 APPLICANT: TATEISHI, NAOKO
 APPLICANT: SENOH, AKIHIRO
 APPLICANT: IKEDA, MASATO
 APPLICANT: OZAKI, AKIO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-125
 CURRENT APPLICATION NUMBER: US/09/738/626
 CURRENT FILING DATE: 2000-12-18
 PRIOR APPLICATION NUMBER: JP 99/377484
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: JP 00/159162
 PRIOR FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: JP 00/280988
 PRIOR FILING DATE: 2000-08-03
 NUMBER OF SEQ ID NOS: 7059
 SOFTWARE: Patent ver. 3.0
 SEQ ID NO 1085
 LENGTH: 1275
 TYPE: DNA
 ORGANISM: Corynebacterium glutamicum
 US-09-738-626-1085

Query Match 80.8%; Score 1275; DB 9; Length 1275;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

151 GTGGCTGAATATATGAGAGCTATGCTGCGGAAATTCGACTCCCGGAGTAAACCAACC 210
 1 GTGGCTGAATATATGAGAGCTATGCTGCGGAAATTCGACTCCCGGAGTAAACCAACC 60
 211 GTGAGAGCAGAGGTTTCTGATGAGGTTTCCACGAGTGTGAGAGGTTCCATCCGCG 270
 61 GTGAGAGCAGAGGTTTCTGATGAGGTTTCCACGAGTGTGAGAGGTTCCATCCGCG 120
 271 GCATCCACCGGCTCCACGAGCTCATGAGCTGCTGAGCGTGTGAGTGTGATGCTGAGGC 330
 121 GCATCCACCGGCTCCACGAGCTCATGAGCTGCTGAGCGTGTGAGTGTGATGCTGAGGC 180
 331 AAGGCGTTTGAAGCAGTTGAAAGCTCAACGAAAGAAATGGGAGAGAGCTCGCTGAGC 390
 181 AAGGCGTTTGAAGCAGTTGAAAGCTCAACGAAAGAAATGGGAGAGAGCTCGCTGAGC 240
 391 CTGAGAGCTGAGATGAGGCGCTCATGAGAGCAATGATGATGATGATGATGATGATGATGAT 450
 241 CTGAGAGCTGAGATGAGGCGCTCATGAGAGCAATGATGATGATGATGATGATGATGATGAT 300
 451 AACAGTCCCGCTGAGGCTCAACAGCAATCTTGTGTTTCCATGAGTGTGTTGAAAGCT 510
 301 AACAGTCCCGCTGAGGCTCAACAGCAATCTTGTGTTTCCATGAGTGTGTTGAAAGCT 360
 511 GCTGCTGATTCGCGAGGCTCCACCTGCTTCCGCTACATGAGGAGCAACAGCAAGCT 570
 361 GCTGCTGATTCGCGAGGCTCCACCTGCTTCCGCTACATGAGGAGCAACAGCAAGCT 420
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 421 CTTCCAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 631 GTTCAGGAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 690
 481 GTTCAGGAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 691 GCGCGAGAGCTTACACGACGATGAGTCCGTATCAAGAAAGAGGCTGCTCCAGGAG 750
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 751 CTTGGGATGAGGCGGCTTCTGCTTCCGTGAGCTTCAACCGTGAAGCTTTCGACTT 810

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